<110> KAO CORPORATION
      Keiji Endo
      Katsuya Ozaki

<120> Mutant Bacterium Belonging to the Genus Bacillus

<130> KS0816

<150> JP 2004-062852
<151> 2004-03-05

<160> 28

<170> PatentIn Ver. 3.1

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      35   40   45

Met Asp Glu Tyr Tyr Glu Phe Leu Gly Glu Gln Gly Val Glu Leu Ile
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Ser Glu Asn Glu Glu Thr Glu Asp Pro Asn Ile Gln Gln Leu Ala Lys
65   70   75   80

Ala Glu Glu Glu Phe Asp Leu Asn Asp Leu Ser Val Pro Pro Gly Val
            85   90   95

Lys Ile Asn Asp Pro Val Arg Met Tyr Leu Lys Glu Ile Gly Arg Val
         100   105   110

Asn Leu Leu Ser Ala Lys Glu Glu Ile Ala Tyr Ala Gln Lys Ile Glu
      115   120   125

Glu Gly Asp Glu Glu Ser Lys Arg Arg Leu Ala Glu Ala Asn Leu Arg
    130   135   140

Leu Val Val Ser Ile Ala Lys Arg Tyr Val Gly Arg Gly Met Leu Phe
145   150   155   160

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Leu Asp Leu Ile His Glu Gly Asn Met Gly Leu Met Lys Ala Val Glu
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Lys Phe Asp Tyr Arg Lys Gly Tyr Lys Phe Ser Thr Tyr Ala Thr Trp
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Trp Ile Arg Gln Ala Ile Thr Arg Ala Ile Ala Asp Gln Ala Arg Thr
            195             200             205

Ile Arg Ile Pro Val His Met Val Glu Thr Ile Asn Lys Leu Ile Arg
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Val Gln Arg Gln Leu Leu Gln Asp Leu Gly Arg Glu Pro Thr Pro Glu
225             230             235             240

Glu Ile Ala Glu Asp Met Asp Leu Thr Pro Glu Lys Val Arg Glu Ile
            245             250             255

Leu Lys Ile Ala Gln Glu Pro Val Ser Leu Glu Thr Pro Ile Gly Glu
            260             265             270

Glu Asp Asp Ser His Leu Gly Asp Phe Ile Glu Asp Gln Glu Ala Thr
            275             280             285

Ser Pro Ser Asp His Ala Ala Tyr Glu Leu Leu Lys Glu Gln Leu Glu
    290             295             300

Asp Val Leu Asp Thr Leu Thr Asp Arg Glu Glu Asn Val Leu Arg Leu
305             310             315             320

Arg Phe Gly Leu Asp Asp Gly Arg Thr Arg Thr Leu Glu Glu Val Gly
            325             330             335

Lys Val Phe Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ala Lys
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agtcaccaat ttggcacgga cgttagaaga gatgaaagag cggggaatct gggttgtcgg     240

aacggatgcg tccgcgcgtg aggatttccg taatatggac ggcaatatgc ctttggctct     300

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tacaggaaac agggttattg ttgttttga cgcgcatctc gtaaaagggc ttgagaaaaa      660

acagaccaac catagagttg aagtaatttt tacaaaagaa aatgagacgg ctgatgagcg     720

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ttccgaaaag ccggcgggta aaattgcttt atcggaagag gttttgaaaa cgtttgaaaa     960

gtggaggcgg ggagacttag attaagttga cgctttttg cccaatactg tataatattt      1020

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caaaatcaaa atgagtgata aggtccgtac aagcgagcat gcggcgtcaa tgggcggctc     180

acagatattc cttgagcccg gcgaagaaat gactgtcaaa gaaatgctga aaggcatcgc     240

aatcgcttcg ggaaatgacg cttccgtcgc catggctgaa tttatttccg gctctgaaga     300

agaatttgtg aagaaaatga ataaaaaagc aaaagagctg ggattgaaaa atacatcctt     360

taaaaaccca acaggactga ccgaggaagg acactacagc tctgcttatg acatggcaat     420

catggctaag gaattattga atacgaatc aattacgaag tttaccggca cgtatgaaga     480

ttatctgcgt gaaaatacag ataaaaagtt ttggcttgta aatacaaatc gccttatcaa     540

attttatcct ggtgtagacg gcgtaaaaac aggctataca ggcgaagcga atattgtct      600

gactgcttcg gctaaaaaag gaaacatgcg ggccatagcg gttgtattcg gagcgagcac     660
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gcctaaagaa agaaacgcgc aagtgacaaa aatgcttgac ttcgccttta gccaatatga      720

aacgcatcct ttatataaac gaaatcaaac agtagcaaaa gtaaaggtca aaaaagggaa      780

acaaaaattt atcgaactca ctacatctga gccgatttca atattgacga aaaaaggcga      840

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tcctgttgct gcaaaagaag atatgaagaa agccgggttt atcacattct aaagcggac      1020

gatgggagac tggacaaaat ttaagtaatt atgccgaatg accactagtt ttgtcacggt      1080

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            20                  25                  30


Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
        35                  40                  45


Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
    50                  55                  60


Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met
65                  70                  75                  80


Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro
                85                  90                  95


Glu Leu Ile Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu
            100                 105                 110


Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
            115                 120                 125


Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile
        130                 135                 140
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Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145   150   155   160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
               165   170   175

Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
           180   185   190

Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
       195   200   205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
   210   215   220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225   230   235   240

Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly
               245   250   255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
               260   265   270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro
       275   280   285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
   290   295   300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305   310   315   320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp
               325   330   335

Pro Gly Pro Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly
               340   345   350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
       355   360   365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
   370   375   380

Gln Gly Phe Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala
385   390   395   400

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Val Asp Asn Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser
        405             410             415

Asn Asp Val Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala
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Asn Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr
        435             440             445

Met Asp Val Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile
    450             455             460

Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg
465             470             475             480

Val Asn Ala Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala
            485             490             495

Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala
        500             505             510

Phe His Glu Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly
        515             520             525

Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly
    530             535             540

Thr Glu Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val
545             550             555             560

Leu Pro Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala
            565             570             575

Gly Glu Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly
        580             585             590

Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser
        595             600             605

Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu
    610             615             620

Val Arg Gly Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro
625             630             635             640

Val Arg Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro
            645             650             655
                          Page 6
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Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn
            660             665         670

Phe Asp Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr
            675             680             685

Glu Val Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr
    690             695             700

Leu Leu Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe
705             710             715             720

Ala Gly Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr
            725             730             735

Thr Glu Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro
            740             745             750

Pro Val Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys
            755             760             765

Glu Glu Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu
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Lys Lys Ala Val Lys Asn Glu Ala Lys Lys Lys
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gaaataaaag tagaagacaa aggacataag aaaattgcat tagtttttaat tatagaaaac     180
gccttttttat aattatttat acctagaacg aaaatactgt ttcgaaagcg gtttactata     240
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aaaccttata ttccggctct tttttaaaac aggggggtaaa aattcactct agtattctaa          300

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gtaagcggtt aaccttgtgc tatatgccga tttaggaagg ggggtagatt gagtcaagta          420

gtaataatat agataactta taagttgttg agaagcagga gagcatctgg gttactcaca          480

agtttttta aaactttaac gaaagcactt tcggtaatgc ttatgaattt agctatttga           540

ttcaattact ttaaaaatat ttaggaggta at atg atg tta aga aag aaa aca            593
                                   Met Met Leu Arg Lys Lys Thr
                                                       -25

aag cag ttg att tct tcc att ctt att tta gtt tta ctt cta tct tta           641
Lys Gln Leu Ile Ser Ser Ile Leu Ile Leu Val Leu Leu Leu Ser Leu
        -20             -15                 -10

ttt ccg gca gct ctt gca gca gaa gga aac act cgt gaa gac aat ttt           689
Phe Pro Ala Ala Leu Ala Ala Glu Gly Asn Thr Arg Glu Asp Asn Phe
    -5           -1  1                 5                       10

aaa cat tta tta ggt aat gac aat gtt aaa cgc cct tct gag gct ggc           737
Lys His Leu Leu Gly Asn Asp Asn Val Lys Arg Pro Ser Glu Ala Gly
                15              20              25

gca tta caa tta caa gaa gtc gat gga caa atg aca tta gta gat caa           785
Ala Leu Gln Leu Gln Glu Val Asp Gly Gln Met Thr Leu Val Asp Gln
            30              35              40

cat gga gaa aaa att caa tta cgt gga atg agt aca cac gga tta cag           833
His Gly Glu Lys Ile Gln Leu Arg Gly Met Ser Thr His Gly Leu Gln
            45              50              55

tgg ttt cct gag atc ttg aat gat aac gca tac aaa gct ctt tct aac           881
Trp Phe Pro Glu Ile Leu Asn Asp Asn Ala Tyr Lys Ala Leu Ser Asn
60                  65              70

gat tgg gat tcc aat atg att cgt ctt gct atg tat gta ggt gaa aat          929
Asp Trp Asp Ser Asn Met Ile Arg Leu Ala Met Tyr Val Gly Glu Asn
75                  80              85              90

ggg tac gct aca aac cct gag tta atc aaa caa aga gtg att gat gga         977
Gly Tyr Ala Thr Asn Pro Glu Leu Ile Lys Gln Arg Val Ile Asp Gly
                95              100             105

att gag tta gcg att gaa aat gac atg tat gtt att gtt gac tgg cat          1025
Ile Glu Leu Ala Ile Glu Asn Asp Met Tyr Val Ile Val Asp Trp His
            110             115             120

gtt cat gcg cca ggt gat cct aga gat cct gtt tat gca ggt gct aaa         1073
Val His Ala Pro Gly Asp Pro Arg Asp Pro Val Tyr Ala Gly Ala Lys
            125             130             135

gat ttc ttt aga gaa att gca gct tta tac cct aat aat cca cac att         1121
Asp Phe Phe Arg Glu Ile Ala Ala Leu Tyr Pro Asn Asn Pro His Ile
            140             145             150

att tat gag tta gcg aat gag ccg agt agt aat aat aat ggt gga gca         1169
Ile Tyr Glu Leu Ala Asn Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala
155                 160             165             170
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ggg att ccg aat aac gaa gaa ggt tgg aaa gcg gta aaa gaa tat gct      1217
Gly Ile Pro Asn Asn Glu Glu Gly Trp Lys Ala Val Lys Glu Tyr Ala
            175                 180                 185

gat cca att gta gaa atg tta cgt aaa agc ggt aat gca gat gac aac      1265
Asp Pro Ile Val Glu Met Leu Arg Lys Ser Gly Asn Ala Asp Asp Asn
            190                 195                 200

att atc att gtt ggt agt cca aac tgg agt cag cgt ccg gac tta gca      1313
Ile Ile Ile Val Gly Ser Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala
            205                 210                 215

gct gat aat cca att gat gat cac cat aca atg tat act gtt cac ttc      1361
Ala Asp Asn Pro Ile Asp Asp His His Thr Met Tyr Thr Val His Phe
    220                 225                 230

tac act ggt tca cat gct gct tca act gaa agc tat ccg tct gaa act      1409
Tyr Thr Gly Ser His Ala Ala Ser Thr Glu Ser Tyr Pro Ser Glu Thr
235                 240                 245                 250

cct aac tct gaa aga gga aac gta atg agt aac act cgt tat gcg tta      1457
Pro Asn Ser Glu Arg Gly Asn Val Met Ser Asn Thr Arg Tyr Ala Leu
                255                 260                 265

gaa aac gga gta gcg gta ttt gca aca gag tgg gga acg agt caa gct      1505
Glu Asn Gly Val Ala Val Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala
                270                 275                 280

agt gga gac ggt ggt cct tac ttt gat gaa gca gat gta tgg att gaa      1553
Ser Gly Asp Gly Gly Pro Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu
            285                 290                 295

ttt tta aat gaa aac aac att agc tgg gct aac tgg tct tta acg aat      1601
Phe Leu Asn Glu Asn Asn Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn
    300                 305                 310

aaa aat gaa gta tct ggt gca ttt aca cca ttc gag tta ggt aag tct      1649
Lys Asn Glu Val Ser Gly Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser
315                 320                 325                 330

aac gca acc aat ctt gac cca ggt cca gat cat gtg tgg gca cca gaa      1697
Asn Ala Thr Asn Leu Asp Pro Gly Pro Asp His Val Trp Ala Pro Glu
                335                 340                 345

gaa tta agt ctt tct gga gaa tat gta cgt gct cgt att aaa ggt gtg      1745
Glu Leu Ser Leu Ser Gly Glu Tyr Val Arg Ala Arg Ile Lys Gly Val
                350                 355                 360

aac tat gag cca atc gac cgt aca aaa tac acg aaa gta ctt tgg gac      1793
Asn Tyr Glu Pro Ile Asp Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp
            365                 370                 375

ttt aat gat gga acg aag caa gga ttt gga gtg aat tcg gat tct cca      1841
Phe Asn Asp Gly Thr Lys Gln Gly Phe Gly Val Asn Ser Asp Ser Pro
    380                 385                 390

aat aaa gaa ctt att gca gtt gat aat gaa aac aac act ttg aaa gtt      1889
Asn Lys Glu Leu Ile Ala Val Asp Asn Glu Asn Asn Thr Leu Lys Val
395                 400                 405                 410

tcg gga tta gat gta agt aac gat gtt tca gat ggc aac ttc tgg gct      1937
Ser Gly Leu Asp Val Ser Asn Asp Val Ser Asp Gly Asn Phe Trp Ala
            415                 420                 425
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aat gct cgt ctt tct gcc aac ggt tgg gga aaa agt gtt gat att tta      1985
Asn Ala Arg Leu Ser Ala Asn Gly Trp Gly Lys Ser Val Asp Ile Leu
            430                 435                 440

ggt gct gag aag ctt aca atg gat gtt att gtt gat gaa cca acg acg      2033
Gly Ala Glu Lys Leu Thr Met Asp Val Ile Val Asp Glu Pro Thr Thr
            445                 450                 455

gta gct att gcg gcg att cca caa agt agt aaa agt gga tgg gca aat      2081
Val Ala Ile Ala Ala Ile Pro Gln Ser Ser Lys Ser Gly Trp Ala Asn
            460                 465                 470

cca gag cgt gct gtt cga gtg aac gcg gaa gat ttt gtc cag caa acg      2129
Pro Glu Arg Ala Val Arg Val Asn Ala Glu Asp Phe Val Gln Gln Thr
475                 480                 485                 490

gac ggt aag tat aaa gct gga tta aca att aca gga gaa gat gct cct      2177
Asp Gly Lys Tyr Lys Ala Gly Leu Thr Ile Thr Gly Glu Asp Ala Pro
                495                 500                 505

aac cta aaa aat atc gct ttt cat gaa gaa gat aac aat atg aac aac      2225
Asn Leu Lys Asn Ile Ala Phe His Glu Glu Asp Asn Asn Met Asn Asn
            510                 515                 520

atc att ctg ttc gtg gga act gat gca gct gac gtt att tac tta gat      2273
Ile Ile Leu Phe Val Gly Thr Asp Ala Ala Asp Val Ile Tyr Leu Asp
            525                 530                 535

aac att aaa gta att gga aca gaa gtt gaa att cca gtt gtt cat gat      2321
Asn Ile Lys Val Ile Gly Thr Glu Val Glu Ile Pro Val Val His Asp
            540                 545                 550

cca aaa gga gaa gct gtt ctt cct tct gtt ttt gaa gac ggt aca cgt      2369
Pro Lys Gly Glu Ala Val Leu Pro Ser Val Phe Glu Asp Gly Thr Arg
555                 560                 565                 570

caa ggt tgg gac tgg gct gga gag tct ggt gtg aaa aca gct tta aca      2417
Gln Gly Trp Asp Trp Ala Gly Glu Ser Gly Val Lys Thr Ala Leu Thr
                575                 580                 585

att gaa gaa gca aac ggt tct aac gcg tta tca tgg gaa ttt gga tat      2465
Ile Glu Glu Ala Asn Gly Ser Asn Ala Leu Ser Trp Glu Phe Gly Tyr
            590                 595                 600

cca gaa gta aaa cct agt gat aac tgg gca aca gct cca cgt tta gat      2513
Pro Glu Val Lys Pro Ser Asp Asn Trp Ala Thr Ala Pro Arg Leu Asp
            605                 610                 615

ttc tgg aaa tct gac ttg gtt cgc ggt gag aat gat tat gta gct ttt      2561
Phe Trp Lys Ser Asp Leu Val Arg Gly Glu Asn Asp Tyr Val Ala Phe
    620                 625                 630

gat ttc tat cta gat cca gtt cgt gca aca gaa ggc gca atg aat atc      2609
Asp Phe Tyr Leu Asp Pro Val Arg Ala Thr Glu Gly Ala Met Asn Ile
635                 640                 645                 650

aat tta gta ttc cag cca cct act aac ggg tat tgg gta caa gca cca      2657
Asn Leu Val Phe Gln Pro Pro Thr Asn Gly Tyr Trp Val Gln Ala Pro
                655                 660                 665

aaa acg tat acg att aac ttt gat gaa tta gag gaa gcg aat caa gta      2705
Lys Thr Tyr Thr Ile Asn Phe Asp Glu Leu Glu Glu Ala Asn Gln Val
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                670                    675                    680
aat ggt tta tat cac tat gaa gtg aaa att aac gta aga gat att aca      2753
Asn Gly Leu Tyr His Tyr Glu Val Lys Ile Asn Val Arg Asp Ile Thr
        685                590                    695

aac att caa gat gac acg tta cta cgt aac atg atg atc att ttt gca      2801
Asn Ile Gln Asp Asp Thr Leu Leu Arg Asn Met Met Ile Ile Phe Ala
    700                705                    710

gat gta gaa agt gac ttt gca ggg aga gtc ttt gta gat aat gtt cgt      2849
Asp Val Glu Ser Asp Phe Ala Gly Arg Val Phe Val Asp Asn Val Arg
715                720                    725                    730

ttt gag ggg gct gct act act gag ccg gtt gaa cca gag cca gtt gat      2897
Phe Glu Gly Ala Ala Thr Thr Glu Pro Val Glu Pro Glu Pro Val Asp
                735                    740                    745

cct ggc gaa gag acg cca cct gtc gat gag aag gaa gcg aaa aaa gaa      2945
Pro Gly Glu Glu Thr Pro Pro Val Asp Glu Lys Glu Ala Lys Lys Glu
                750                    755                    760

caa aaa gaa gca gag aaa gaa gag aaa gaa gca gta aaa gaa gaa aag      2993
Gln Lys Glu Ala Glu Lys Glu Glu Lys Glu Ala Val Lys Glu Glu Lys
        765                    770                    775

aaa gaa gct aaa gaa gaa aag aaa gca gtc aaa aat gag gct aag aaa      3041
Lys Glu Ala Lys Glu Glu Lys Lys Ala Val Lys Asn Glu Ala Lys Lys
    780                    785                    790

aaa taatctatta aactagttat agggttatct aaaggtctga tgtagatctt           3094
Lys
795

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            20                  25                  30

Val Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln
        35                  40                  45

Leu Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu
    50                  55                  60

Asn Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met
65                  70                  75                  80
```

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Ile Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro
             85              90          95

Glu Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu
            100             105             110

Asn Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp
            115             120             125

Pro Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile
    130             135             140

Ala Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn
145             150             155             160

Glu Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu
                165             170             175

Glu Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met
            180             185             190

Leu Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser
    195             200             205

Pro Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp
210             215             220

Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
225             230             235             240

Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
            245             250             255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
            260             265             270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
    275             280             285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
    290             295             300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
305             310             315             320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp
            325             330             335
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Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly
340   345   350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
355   360   365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
370   375   380

Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile
385   390   395   400

Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn
405   410   415

Asp Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp
420   425   430

Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met
435   440   445

Asp Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro
450   455   460

Gln Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val
465   470   475   480

Glu Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu
485   490   495

Thr Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His
500   505   510

Ala Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu
515   520   525

Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu
530   535   540

Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro
545   550   555   560

Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu
565   570   575

Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn
                        Page 13

                    580   585   590

Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn
        595   600   605

Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg
    610   615   620

Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg
625   630   635   640

Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr
            645   650   655

Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp
            660   665   670

Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val
        675   680   685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
    690   695   700

Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly
705   710   715   720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
                725   730   735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
            740   745   750

Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu
        755   760   765

Lys Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys
    770   775   780

Ala Ile Lys Asn Glu Ala Thr Lys Lys
785   790

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cttatattta gagggaattt cttttttaaat tgaatacgga ataaaatcag gtaaacaggt     120

cctgatttta ttttttttgaa ttttttttgag aactaaagat tgaaatagaa gtagaagaca    180

acggacataa gaaaattgta ttagtttttaa ttatagaaaa cgcttttcta taattattta     240

tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc      300

tttttttaaa caggggggtga aaattcactc tagtattcta atttcaacat gctataataa     360

atttgtaaga cgcaatatac atcttttttt tatgatattt gtaagcggtt aaccttgtgc      420

tatatgccga tttaggaagg gggtagattg agtcaagtag tcataattta gataacttat      480

aagttgttga gaagcaggag agaatctggg ttactcacaa gttttttaaa acattatcga      540

aagcactttc ggttatgctt atgaatttag ctatttgatt caattacttt aataatttta     600
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ggaggtaat atg atg tta aga aag aaa aca aag cag ttg att tct tcc att     651
           Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile
                        -25                  -20

ctt att tta gtt tta ctt cta tct tta ttt ccg aca gct ctt gca gca     699
Leu Ile Leu Val Leu Leu Leu Ser Leu Phe Pro Thr Ala Leu Ala Ala
-15              -10                  -5                  -1  1

gaa gga aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat gac     747
Glu Gly Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp
            5                  10                  15

aat gtt aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc     795
Asn Val Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val
        20                  25                  30

gat gga caa atg aca tta gta gat caa cat gga gaa aaa att caa tta     843
Asp Gly Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu
    35                  40                  45

cgt gga atg agt aca cac gga tta caa tgg ttt cct gag atc ttg aat     891
Arg Gly Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn
50                  55                  60                  65

gat aac gca tac aaa gct ctt gct aac gat tgg gaa tca aat atg att     939
Asp Asn Ala Tyr Lys Ala Leu Ala Asn Asp Trp Glu Ser Asn Met Ile
                70                  75                  80

cgt cta gct atg tat gtc ggt gaa aat ggc tat gct tca aat cca gag     987
Arg Leu Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Ser Asn Pro Glu
            85                  90                  95

tta att aaa agc aga gtc att aaa gga ata gat ctt gct att gaa aat    1035
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Leu Ile Lys Ser Arg Val Ile Lys Gly Ile Asp Leu Ala Ile Glu Asn
        100             105             110

gac atg tat gtc atc gtt gat tgg cat gta cat gca cct ggt gat cct      1083
Asp Met Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro
        115             120             125

aga gat ccc gtt tac gct gga gca gaa gat ttc ttt aga gat att gca      1131
Arg Asp Pro Val Tyr Ala Gly Ala Glu Asp Phe Phe Arg Asp Ile Ala
130             135             140             145

gca tta tat cct aac aat cca cac att att tat gag tta gcg aat gag      1179
Ala Leu Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu
                150             155             160

cca agt agt aac aat aat ggt gga gct ggg att cca aat aat gaa gaa      1227
Pro Ser Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu
                165             170             175

ggt tgg aat gcg gta aaa gaa tac gct gat cca att gta gaa atg tta      1275
Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu
                180             185             190

cgt gat agc ggg aac gca gat gac aat att atc att gtg ggt agt cca      1323
Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro
        195             200             205

aac tgg agt cag cgt cct gac tta gca gct gat aat cca att gat gat      1371
Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp
210             215             220             225

cac cat aca atg tat act gtt cac ttc tac act ggt tca cat gct gct      1419
His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala
                230             235             240

tca act gaa agc tat ccg cct gaa act cct aac tct gaa aga gga aac      1467
Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn
                245             250             255

gta atg agt aac act cgt tat gcg tta gaa aac gga gta gca gta ttt      1515
Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe
                260             265             270

gca aca gag tgg gga act agc caa gca aat gga gat ggt ggt cct tac      1563
Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro Tyr
        275             280             285

ttt gat gaa gca gat gta tgg att gag ttt tta aat gaa aac aac att      1611
Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile
290             295             300             305

agc tgg gct aac tgg tct tta acg aat aaa aat gaa gta tct ggt gca      1659
Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala
                310             315             320

ttt aca cca ttc gag tta ggt aag tct aac gca aca agt ctt gac cca      1707
Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp Pro
                325             330             335

ggg cca gac caa gta tgg gta cca gaa gag tta agt ctt tct gga gaa      1755
Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly Glu
        340             345             350
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tat gta cgt gct cgt att aaa ggt gtg aac tat gag cca atc gac cgt          1803
Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg
355             360             365

aca aaa tac acg aaa gta ctt tgg gac ttt aat gat gga acg aag caa          1851
Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln
370             375             380             385

gga ttt gga gtg aat gga gat tct cca gtt gaa gat gta gtt att gag          1899
Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu
                390             395             400

aat gaa gcg ggc gct tta aaa ctt tca gga tta gat gca agt aat gat          1947
Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn Asp
            405             410             415

gtt tct gaa ggt aat tac tgg gct aat gct cgt ctt tct gcc gac ggt          1995
Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp Gly
            420             425             430

tgg gga aaa agt gtt gat att tta ggt gct gaa aaa ctt act atg gat          2043
Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp
    435             440             445

gtg att gtt gat gag ccg acc acg gta tca att gct gca att cca caa          2091
Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro Gln
450             455             460             465

ggg cca tca gcc aat tgg gtt aat cca aat cgt gca att aag gtt gag          2139
Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val Glu
                470             475             480

cca act aat ttc gta ccg tta gga gat aag ttt aaa gcg gaa tta act          2187
Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu Thr
                485             490             495

ata act tca gct gac tct cca tcg tta gaa gct att gcg atg cat gct          2235
Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His Ala
            500             505             510

gaa aat aac aac atc aac aac atc att ctt ttt gta gga act gaa ggt          2283
Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu Gly
    515             520             525

gct gat gtt atc tat tta gat aac att aaa gta att gga aca gaa gtt          2331
Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val
530             535             540             545

gaa att cca gtt gtt cat gat cca aaa gga gaa gct gtt ctt cct tct          2379
Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser
                550             555             560

gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct gga gag tct          2427
Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser
            565             570             575

ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt tct aac gcg          2475
Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala
    580             585             590

tta tca tgg gaa ttt gga tac cca gaa gta aaa cct agt gat aac tgg          2523
Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp
    595             600             605
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gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt        2571
Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly
610                 615                 620                 625

gaa aat gat tat gta act ttt gat ttc tat cta gat cca gtt cgt gca        2619
Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala
                630                 635                 640

aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac        2667
Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn
            645                 650                 655

ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa        2715
Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu
        660                 665                 670

tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa        2763
Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys
    675                 680                 685

att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt        2811
Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg
690                 695                 700                 705

aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga        2859
Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg
                710                 715                 720

gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg        2907
Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro
            725                 730                 735

gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat        2955
Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp
        740                 745                 750

gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa        3003
Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys
    755                 760                 765

gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca        3051
Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala
770                 775                 780                 785

atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct       3105
Ile Lys Asn Glu Ala Thr Lys Lys
                790

aaaggtctga tgcagatctt ttagataacc tttttttgca taactggaca tagaatggtt      3165

attaaagaaa gcaaggtgtt tatacgatat taaaaggta gcgattttaa attgaaacct        3225

ttaataatgt cttgtgatag aatgatgaag taatttaaga gggggaaacg aagtgaaaac      3285

ggaaatttct agtagaagaa aaacagacca agaaatactg caagctt                    3332
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        sigA in Bacillus subtilis

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<210> 9
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<220>
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         sigA in Bacillus subtilis

<400> 9
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<210> 10
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         the upstream region of sigH in Bacillus subtilis

<400> 10
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 upstream region of sigH in Bacillus subtilis; 5'-portion from nucleotide
sequence of sigA in Bacillus subtilis

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         the upstream region of sigF in Bacillus subtilis

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<220>
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the upstream region of sigF in Bacillus subtilis;
5'-portion from sigA in Bacillus subtilis

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<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer designed from nucleotide sequence of
plasmid pC194

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caactaaagc acccattag 19

<210> 15
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<212> DNA
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<220>
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5'-portion from sigA in Bacillus subtilis

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<223> Oligonucleotide as PCR primer from nucleotide sequence of
sigA in Bacillus subtilis; the sequence containing a nucleotide
substitution for destroying the initiation codon of sigA

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<210> 17
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<212> DNA
<213> artificial sequence

<220>
<223> Oligonucleotide as PCR primer; 3'-portion from the upstream region of sigF
and 5'-portion from sigA in Bacillus subtilis; the sequence containing a
nucleotide substitution for destroying the initiation codon of sigA

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cgatgcgcaa aactgcgcaa ctactagcac tcttcaggga ctaaaccacc tttttttccaa        120

aaatgacatc atataaacaa atttgtctac caatcactat ttaaagctgt ttatgatata         180

tgtaagcgtt atcattaaaa ggaggtattt g atg aga aga tgg gta gta gca             232
                                    Met Arg Arg Trp Val Val Ala
                                    -20                      -15

atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca gat gga           280
Met Leu Ala Val Leu Phe Leu Phe Pro Ser Val Val Val Ala Asp Gly
            -10                   -5                   -1   1

ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa aac gac           328
Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp
          5                   10                  15

ggg cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg agt gat           376
Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu Ser Asp
      20                  25                  30

gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt aat agt           424
Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser
35                  40                  45                  50

cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag           472
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
                  55                  60                  65

ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag gca cag           520
Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln
              70                  75                  80

ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat gta tac           568
Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr
          85                  90                  95

gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg gag gca           616
Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr Glu Ala
100                 105                 110
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gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat att tca          664
Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp Ile Ser
115             120             125             130

ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca ggg cgt          712
Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg
            135             140             145

aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt aat ggt          760
Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly
            150             155             160

gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc ttt gca          808
Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala
            165             170             175

aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat tat gat          856
Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn Tyr Asp
180             185             190

tac ctg tta gga tcg aat atc gac ttt agt cat cca gaa gta caa gat          904
Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp
195             200             205             210

gag ttg aag gat tgg ggt agc tgg ttt acc gat gag tta gat ttg gat          952
Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp Leu Asp
            215             220             225

ggt tat cgt tta gat gct att aaa cat att cca ttc tgg tat aca tct          1000
Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr Thr Ser
            230             235             240

gat tgg gtt cgg cat cag cgc aac gaa gca gat caa gat tta ttt gtc          1048
Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu Phe Val
            245             250             255

gta ggg gaa tat tgg aag gat gac gta ggt gct ctc gaa ttt tat tta          1096
Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe Tyr Leu
260             265             270

gat gaa atg aat tgg gag atg tct cta ttc gat gtt cca ctt aat tat          1144
Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu Asn Tyr
275             280             285             290

aat ttt tac cgg gct tca caa caa ggt gga agc tat gat atg cgt aat          1192
Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met Arg Asn
            295             300             305

att tta cga gga tct tta gta gaa gcg cat ccg atg cat gca gtt acg          1240
Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala Val Thr
            310             315             320

ttt gtt gat aat cat gat act cag cca ggg gag tca tta gag tca tgg          1288
Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu Ser Trp
            325             330             335

gtt gct gat tgg ttt aag cca ctt gct tat gcg aca att ttg acg cgt          1336
Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu Thr Arg
            340             345             350

gaa ggt ggt tat cca aat gta ttt tac ggt gat tac tat ggg att cct          1384
Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly Ile Pro
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      355                     360                     365                     370

aac gat aac att tca gct aaa aaa gat atg att gat gag ctg ctt gat        1432
Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu Leu Asp
            375                 380                 385

gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt gat cat        1480
Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His
            390                 395                 400

tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga cct aat        1528
Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg Pro Asn
            405                 410                 415

tca ggc ctt gcg act att atg tcg aat gga cct ggt ggt tcc aag tgg        1576
Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp
    420                 425                 430

atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat tta act        1624
Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr
435                 440                 445                 450

ggt aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa        1672
Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu
                455                 460                 465

ttc ttt acg aat gga gga tct gta tcc gtg tac gtg aac caa taacaaaaa     1723
Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
                470                 475                 480

gccttgagaa gggattcctc cctaactcaa ggctttcttt atgtcgctta gctttacgct      1783

tctacgactt tg                                                          1795


<210>   19
<211>   480
<212>   PRT
<213>   Bacillus sp. KSM-K38

<400>   19

Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
1               5                   10                  15


Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
                20                  25                  30


Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
        35                  40                  45


Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
    50                  55                  60


Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65                  70                  75                  80


Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
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                  85                    90                    95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
            100                 105                 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
            115                 120                 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
    130                 135                 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145                 150                 155                 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
                165                 170                 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
            180                 185                 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
    195                 200                 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
    210                 215                 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225                 230                 235                 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
                245                 250                 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
            260                 265                 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
    275                 280                 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
    290                 295                 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305                 310                 315                 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
                325                 330                 335
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Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
        340             345                 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
        355                 360                 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
    370                 375                 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385                 390                 395                 400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
                405                 410                 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
                420                 425                 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
        435                 440                 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
    450                 455                 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465                 470                 475                 480


<210>   20
<211>   1441
<212>   DNA
<213>   Bacillus clausii KSM-K16

<220>
<221>   CDS
<222>   (164)..(1303)

<400>   20
tggtagcttt ccccacttga aaccgtttta atcaaaaaac aaagtgggaa aattctgtta       60

acttaatgtt aataattgtt tcccaatagg caaatctttc taactttgat acgtttaaac      120

taccagcttg gacgagttgg gataaaagtg aggagggaac cga atg aag aaa ccg      175
                                               Met Lys Lys Pro
                                               1

ttg ggg aaa att gtc gca agc acc gca cta ctc att tct gtt gct ttt      223
Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile Ser Val Ala Phe
5              10                  15                  20

agt tca tcg atc gca tcg gct gct gag gaa gca aaa gaa aaa tat tta      271
Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys Glu Lys Tyr Leu
            25                  30                  35

att ggc ttt aat gag cag gaa gca gtt agt gag ttt gta gag caa ata      319
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Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe Val Glu Gln Ile
            40                  45              50

gag gca aat gac gat gtc gcg att ctc tct gag gaa gag gaa gtc gaa    367
Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu Glu Glu Val Glu
            55                  60              65

att gaa ttg ctt cat gag ttt gaa acg att cct gtt tta tct gtt gag    415
Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val Leu Ser Val Glu
    70                  75              80

tta agt cca gaa gat gtg gac gcg ctt gag ctc gat cca acg att tcg    463
Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp Pro Thr Ile Ser
85              90                  95              100

tat att gaa gag gat gca gaa gta acg aca atg gcg caa tca gtg cca    511
Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala Gln Ser Val Pro
                105                 110             115

tgg gga att agc cgt gta caa gcc cca gct gcc cat aac cgt gga ttg    559
Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His Asn Arg Gly Leu
            120                 125             130

aca ggt tct ggt gta aaa gtt gct gtc ctc gat acg ggt att tcc acc    607
Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr Gly Ile Ser Thr
            135                 140             145

cat cca gac tta aat att cgc ggt ggt gct agc ttt gtg cca gga gaa    655
His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe Val Pro Gly Glu
    150                 155             160

cca tcc act caa gat gga aat gga cat ggc acg cat gtg gca ggg acg    703
Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His Val Ala Gly Thr
165             170                 175             180

att gct gct tta aac aat tcg att ggc gtt ctg ggc gta gca ccg agc    751
Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ala Pro Ser
                185                 190             195

gcg gaa cta tac gct gta aaa gta tta ggc gcg agc ggt tca ggt tcg    799
Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser Gly Ser Gly Ser
            200                 205             210

gtc agc tcg att gcc caa gga ttg gaa tgg gca ggg aac aat ggc atg    847
Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly Asn Asn Gly Met
            215                 220             225

cac gtt gcg aat ttg agt tta gga agc ccg tcg ccg agt gca aca ctt    895
His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro Ser Ala Thr Leu
    230                 235             240

gag caa gct gtt aat agc gct act tct aga ggc gtt ctt gtc gta gca    943
Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val Leu Val Val Ala
245                 250                 255             260

gca tct ggt aat tca ggt gca ggc tca atc agc tat ccg gcc cgt tat    991
Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr Pro Ala Arg Tyr
            265                 270             275

gcg aac gca atg gca gtc gga gcg act gac caa aac aac aac cgc gct    1039
Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn Asn Asn Arg Ala
            280                 285             290
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agc ttt tca cag tat gga gct ggg ctt gac att gtc gcg cca ggt gtc    1087
Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val Ala Pro Gly Val
        295             300             305

aat gtg cag agc aca tac cca ggt tca aca tat gcc agc tta aac ggt    1135
Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala Ser Leu Asn Gly
    310             315             320

aca tcg atg gct act cct cat gtt gca ggt gta gca gcc ctt gtt aaa    1183
Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala Ala Leu Val Lys
325             330             335             340

caa aag aat cca tct tgg tcc aat gta caa atc cgc aat cat cta aag    1231
Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg Asn His Leu Lys
            345             350             355

aat acg gca acg ggt tta gga aac acg aac ttg tat gga agc ggg ctt    1279
Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr Gly Ser Gly Leu
        360             365             370

gtc aat gca gaa gcg gca aca cgc taatcaataa taataacgct gtgtgcttta    1333
Val Asn Ala Glu Ala Ala Thr Arg
        375             380

agcacacagc gttttttagt gtgtatgaat cgaaaaagag aaatagatcg ctgatttcaa    1393

aaagcgagcg taaagggcta ttgaagctct ttacgcttgc aggatttg               1441
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<210>    21
<211>    380
<212>    PRT
<213>    Bacillus clausii KSM-K16

<400>    21

Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu Ile
1               5               10              15


Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Glu Glu Ala Lys
            20              25              30


Glu Lys Tyr Leu Ile Gly Phe Asn Glu Gln Glu Ala Val Ser Glu Phe
        35              40              45


Val Glu Gln Ile Glu Ala Asn Asp Asp Val Ala Ile Leu Ser Glu Glu
    50              55              60


Glu Glu Val Glu Ile Glu Leu Leu His Glu Phe Glu Thr Ile Pro Val
65              70              75              80


Leu Ser Val Glu Leu Ser Pro Glu Asp Val Asp Ala Leu Glu Leu Asp
            85              90              95


Pro Thr Ile Ser Tyr Ile Glu Glu Asp Ala Glu Val Thr Thr Met Ala
            100             105             110
```

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Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala His
        115             120             125

Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp Thr
        130             135             140

Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser Phe
145             150             155             160

Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr His
            165             170             175

Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly
        180             185             190

Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala Ser
        195             200             205

Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala Gly
210             215             220

Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser Pro
225             230             235             240

Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly Val
            245             250             255

Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser Tyr
            260             265             270

Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln Asn
        275             280             285

Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile Val
        290             295             300

Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr Ala
305             310             315             320

Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Val Ala
            325             330             335

Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile Arg
        340             345             350

Asn His Leu Lys Asn Thr Ala Thr Gly Leu Gly Asn Thr Asn Leu Tyr
        355             360             365
```

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Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
    370                 375             380
```

<210> 22
<211> 46
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer; 3'-portion from
       the alkaline protease gene in Bacillus clausii KSM-K16; 5'-portion from
upstream region of alkaline cellulase gene in Bacillus sp. KSM-S237

<400> 22
actttaaaaa tatttaggag gtaatatgaa gaaaccgttg gggaaa   46

<210> 23
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer designed from the downstream region of the
alkaline protease gene in Bacillus clausii KSM-K16 with a insertion of the
BglII restriction site at the 5'-end

<400> 23
gggagatctt cagcgatcta tttctctttt tc   32

<210> 24
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer designed from the upstream region of the
alkaline cellulase gene in Bacillus sp. KSM-S237 with a insertion of the
BamHI restriction site at the 5'-end

<400> 24
cccggatcca acaggcttat attta   25

<210> 25
<211> 46
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide as PCR primer; 3'-portion from the upstream region of the
 alkaline cellulase gene in Bacillus sp. KSM-S237; 5'-portion designed
from the alkaline protease gene in Bacillus clausii KSM-K16

<400> 25
tttccccaac ggtttcttca tattacctcc taaatatttt taaagt   46

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<210>    26
<211>    30
<212>    DNA
<213>    Artificial

<220>
<223>    Oligonucleotide as PCR primer; 3'-portion from nucleotide
         sequence of the alkaline amylase gene in Bacillus sp. KSM-K
         38; 5'-portion from the alkaline cellulase gene in Bacillus sp. KSM-S237

<400>    26
gctcttgcag cagatggatt gaacggtacg                                    30


<210>    27
<211>    30
<212>    DNA
<213>    Artificial

<220>
<223>    Oligonucleotide as PCR primer designed from the downstream region of the
 alkaline amylase gene in Bacillus sp. KSM-K38 with a insertion of the
XbaI restriction site at the 5'-end

<400>    27
ttggtctaga ccccaagctt caaagtcgta                                    30


<210>    28
<211>    29
<212>    DNA
<213>    Artificial

<220>
<223>    Oligonucleotide as PCR primer; its 3'-portion designed from the alkaline
 cellulase gene in Bacillus sp. KSM -S237 and its 5'-portion designed from        the
alkaline amylase gene in Bacillus sp. KSM-K38

<400>    28
ttcaatccat ctgctgcaag agctgccgg                                     29
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